

Fig. 1

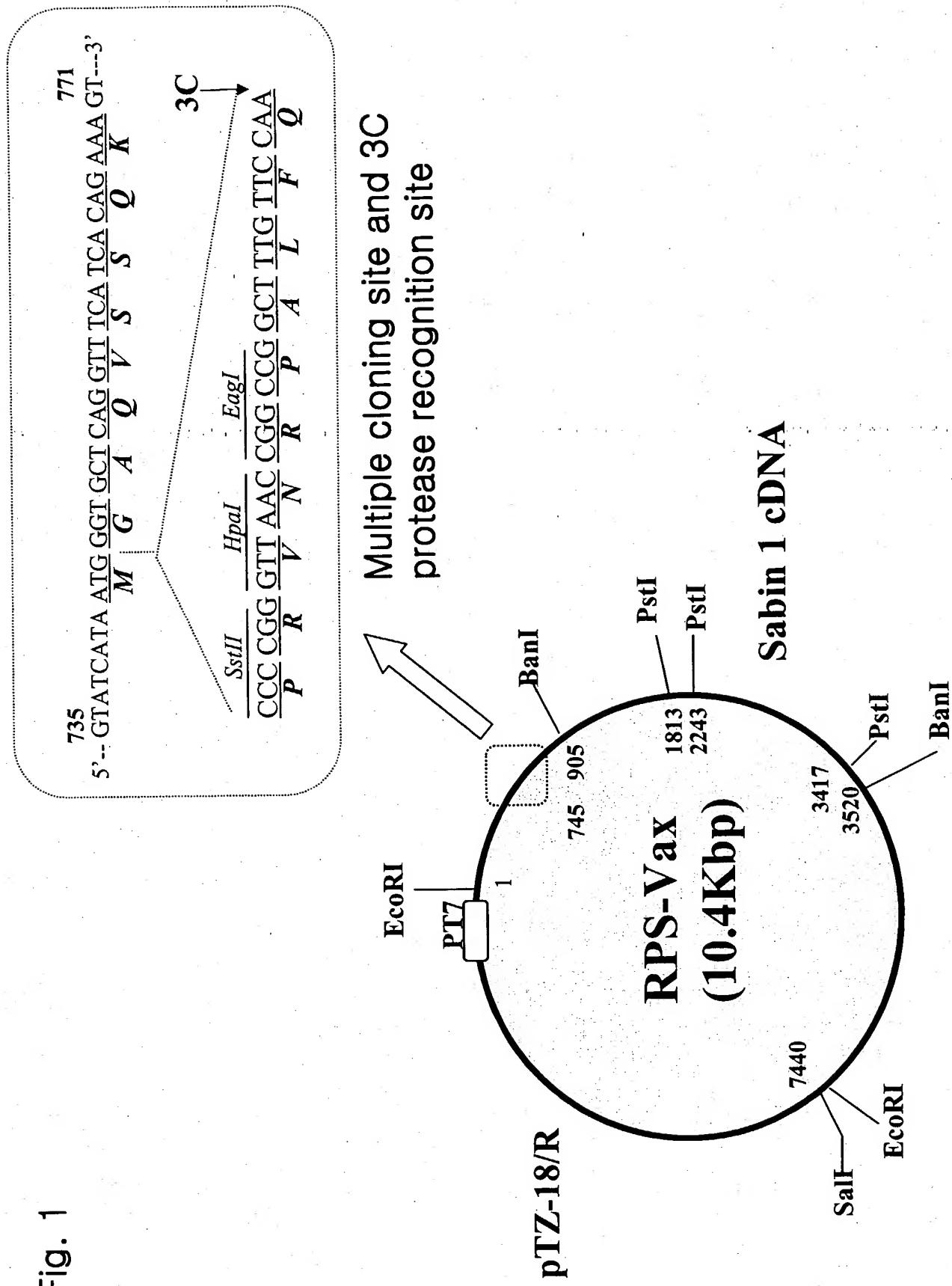


Fig. 2

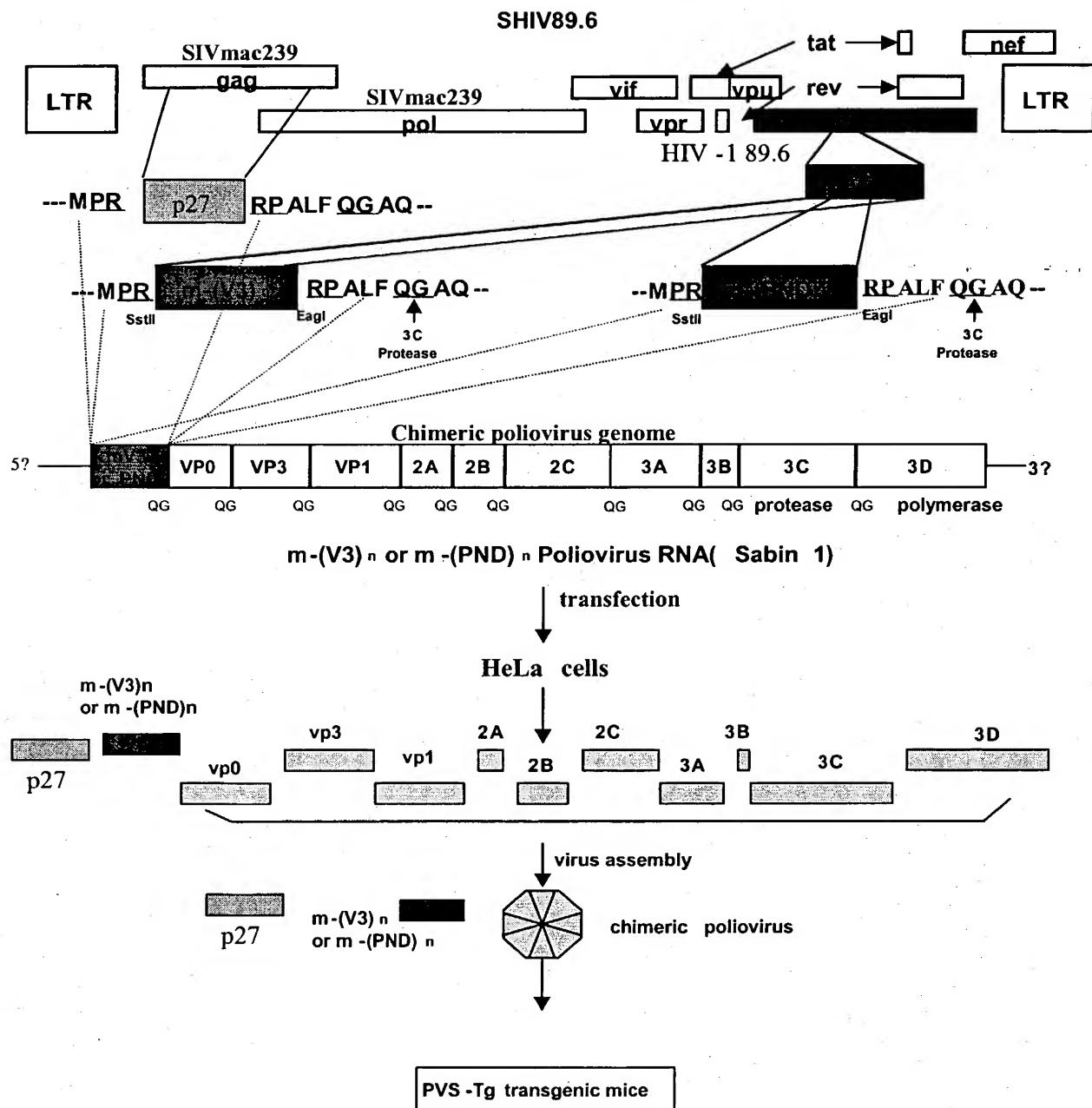


Fig. 3a



Fig. 3b

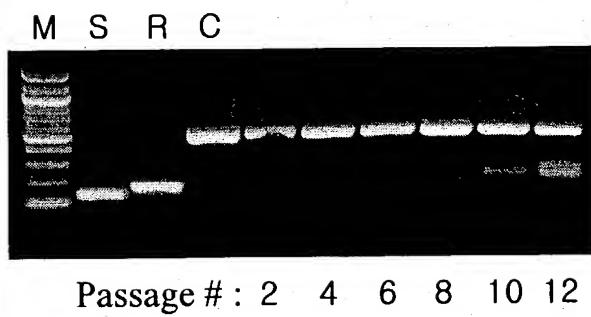


Fig. 3c

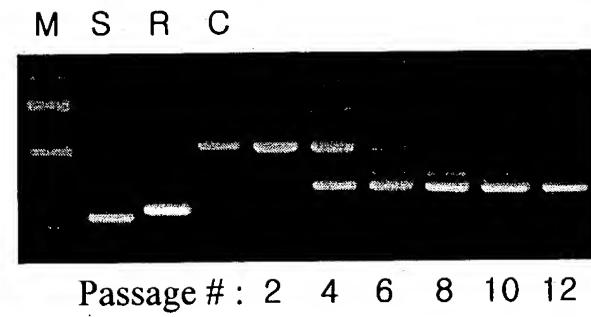


Fig. 5

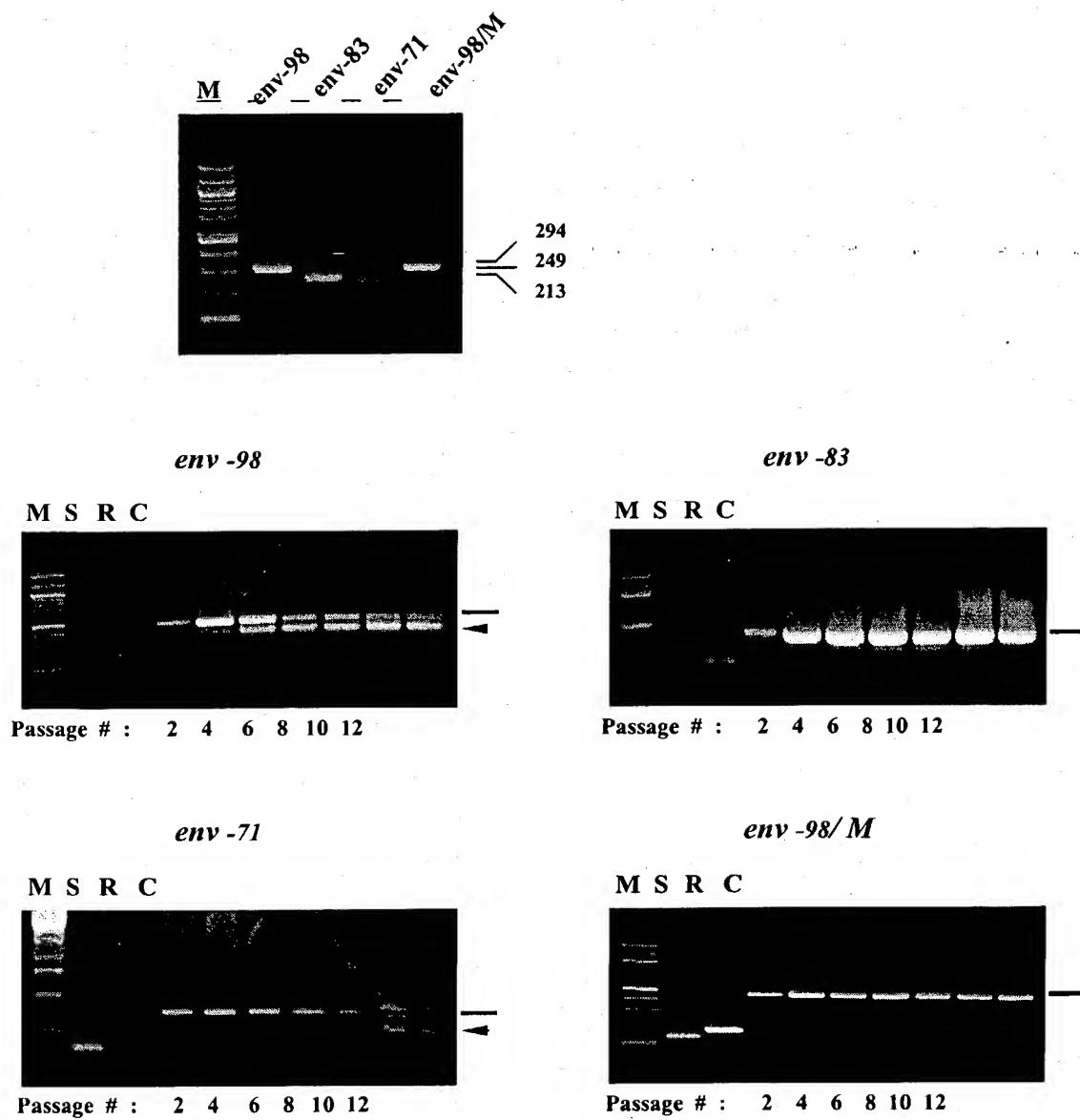


Fig. 4a

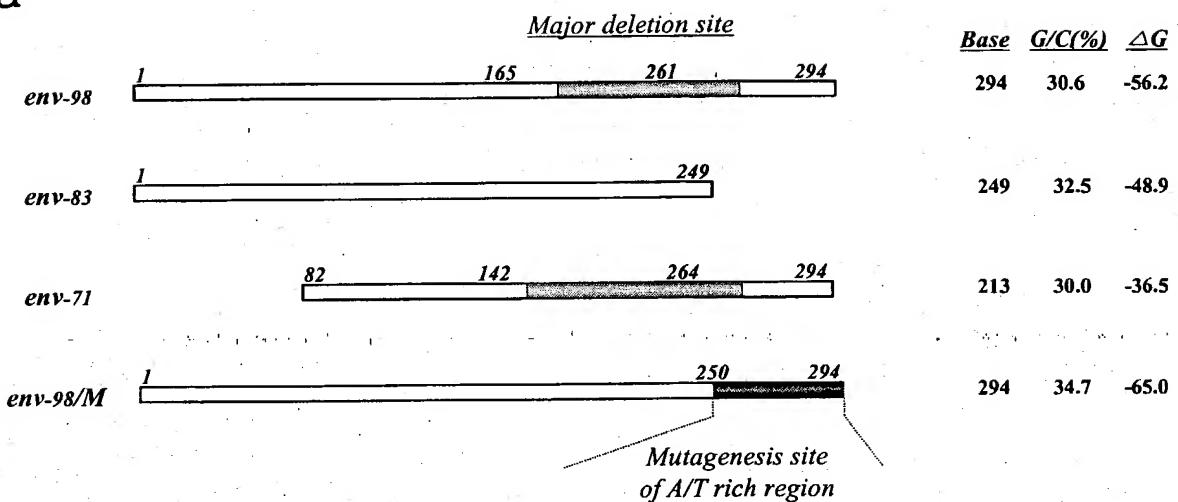


Fig. 4b

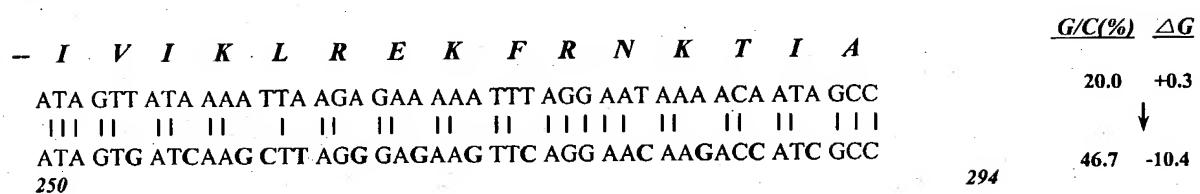


Fig. 4c

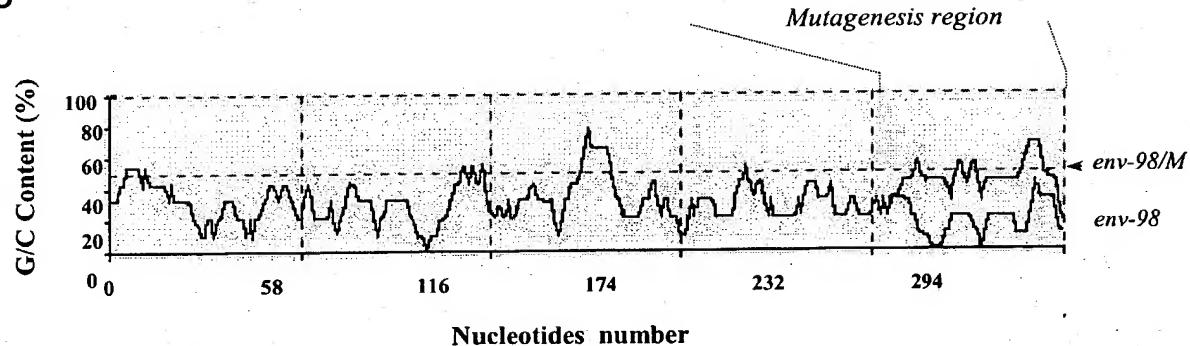


Fig. 6a

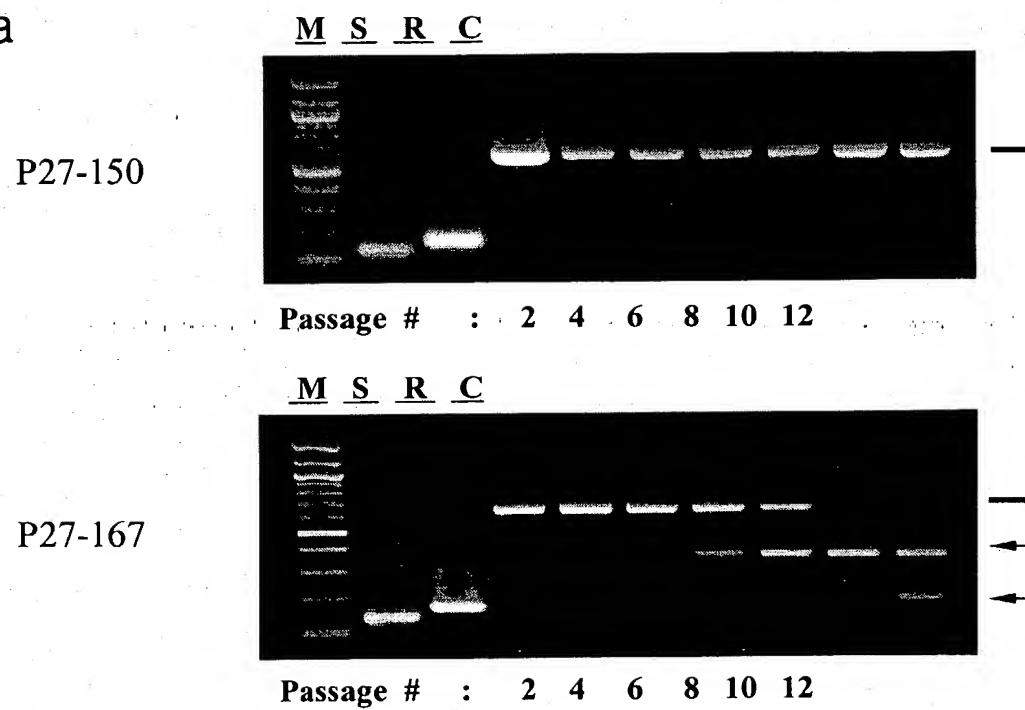


Fig. 6b

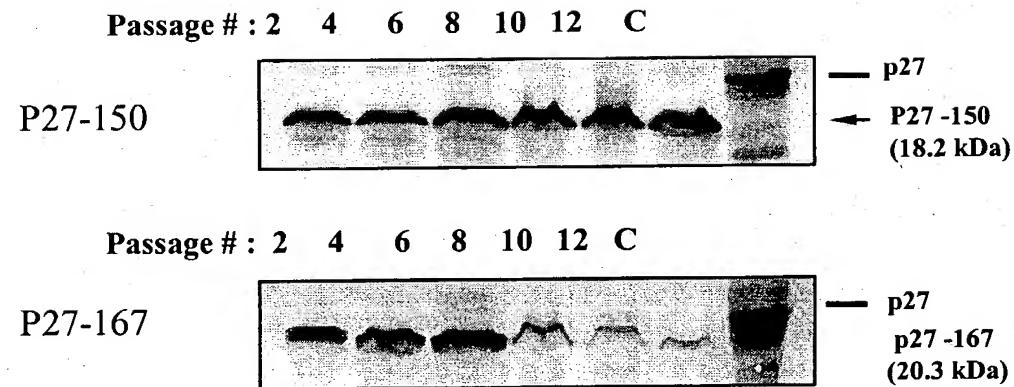


Fig. 7

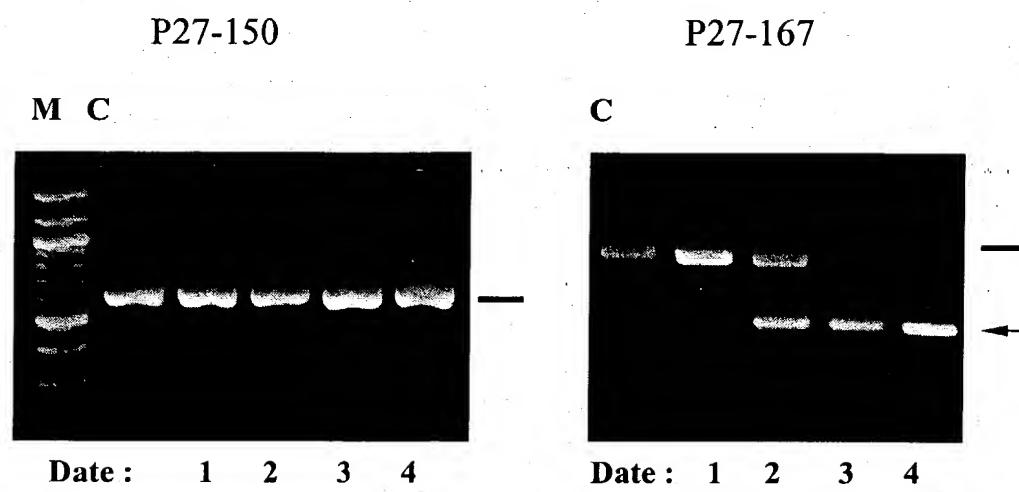


Fig. 8

1	A	K	A	V	A	A	W	T	L	K	A	A	A	G	Q	15
1	GCT	AAG	GCC	GTT	GCA	GCC	TGG	ACC	CTG	AAA	GCC	GCT	GCA	GGC	CAA	45
16	A	S	T	E	G	D	C	G	C	P	A	I	I	E	V	30
46	GCC	TCC	ACC	GAA	GGC	GAC	TGC	GGT	TGC	CCA	<u>GCC</u>	ATC	ATC	GAG	GTC	90
31	D	N	D	A	P	T	K	R	A	S	K	L	F	S	E	45
91	GAT	AAC	GAT	GCC	CCT	ACC	AAG	CGA	GCC	AGC	<u>AAG</u>	CTC	TTC	AGC	GAA	135
	GAT	AAT	GAT	GCT	CCA	ACA	AAG	CGT	GCC	AGT	AAA	TTA				
46	F	E	V	D	N	E	Q	P	T	T	R	A	Q	K	L	60
136	TTC	GAG	GTC	GAT	AAT	GAG	CAG	CCC	ACT	ACC	CGA	GCC	CAG	AAG	CTC	180
	AAT	GAA	CAA	CCA	ACC	ACC	CGG	GCA	CAG	AAA						
61	F	A	M	W	R	I	T	Y	K	D	N	D	A	P	T	75
181	TTC	GCC	ATG	TGG	CGT	ATC	ACT	TAC	AAG	<u>GAC</u>	AAT	GAT	GCG	CCA	ACT	225
	GAT	AAT	GAT	GCT	CCA	ACA										
76	K	R	A	S	K	L	C	V	R	I	Y	M	K	P	K	90
226	AAG	CGC	GCA	TCT	AAA	CTG	TGC	GTC	CGA	ATC	TAC	ATG	AAG	CCC	AAG	270
	AAG	CGT	GCC	AGT	AAA	TTA										
91	H	V	R	C	S	G	C	P	A	I	I	E	V	D	N	105
271	CAC	GTT	CGA	TGC	TCC	GGC	TGT	CCC	<u>GCT</u>	ATT	ATC	GAA	GTG	GAT	AAC	315
	GCC	ATT	ATT	GAA	GTG	GAT	AAT									
106	D	A	P	T	K	R	A	S	K	L	D	N	Y	Q	S	120
316	GAC	GCA	CCA	ACC	AAA	CGG	GCA	TCA	AAG	CTG	GAC	AAC	TAC	CAG	TCC	360
	GAT	GCT	CCA	ACA	AAG	CGT	GCC	AGT	AAA	TTA						
121	P	C	A	I	N	E	Q	P	T	T	R	A	Q	K	S	135
361	CCA	TGC	GCG	ATC	<u>AAC</u>	GAG	CAA	CCT	ACC	ACC	CGT	GCG	CAA	AAG	TCC	405
	AAT	GAA	CAA	CCA	ACC	ACC	CGG	GCA	CAG	AAA						
136	A	G	C	F	Y	Q	T	R	V	V	V	P	S	G	C	150
406	GCT	GGG	TGC	TTC	TAT	CAG	ACC	CGC	GTC	GTG	GTT	CCC	TCA	GGT	TGT	450



: Lansing (wt 2 poliovirus) VP1 neutralizing epitopes.

ori - GCC ATT ATT GAA GTG GAT AAT GAT GCT CCA ACA AAG CGT GCC AGT AAA TTA



: Leon (wt 3 poliovirus) VP1 neutralizing epitopes

ori - AAT GAA CAA CCA ACC ACC CGG GCA CAG AAA CTA



: Coding sequence diversity mediated by application of various codon usage.

Fig. 9

primer 1 →
5-ATTATA CCGCGG
(Sst II)

10 20 30 40 50 60
GCTAAGGCCG TTGCAGCCTG GACCCTGAAA GCCGCTGCAG GCCAAGCCTC CACCGAAGGC
3'-GTGGCTTCCG

primer 3
70 80 90 100 110 120
GACTG-3'
CTGACGCCAA CGGGTCGGTA GTAGCTCCAG CTATTGCTAC GGGGATGGTT CGCTCGGTG-5'
← primer 2

130 140 150 160 170 180
AAGCTCTTCA GCGAATTCGA GGTGATAAT GAGCAGCCCA CTACCCGAGC CCAGA-3'
3'-GATGGGCTCG GGTCTTCGAG

primer 5 →
190 200 210 220 230 240
5'-TGCAG CAACTAAGCG CGCATCTAAA
AAGCGGTACA CCGCATAGTG AATGTTCCCTG TTACTACGCG GTTGATTGCG-5'
← primer 4

250 260 270 280 290 300
CTGTGCGTCC GAATCTACAT GAAGCCCAAG CACGTTCGAT GCTCC-3'
3'-GTGCAAGCTA CGAGGCCGAC AGGGCGATAA

primer 7 →
310 320 330 340 350 360
5'-CCAAA CGGGCATCAA AGCTGGACAA CTACCAGTCC
TAGCTTCACC TATTGCTGCG TGGTTGGTTT GCCCGTAGTT-5'
← primer 6

370 380 390 400 410 420
CCATGCGCGA TCAACCGAGCA ACCTACCACC CGTGC-3'
3'-TGGATGGTGG GCACCGCGTT TCAGGCGACC CACGAAGATA

430 440 450
GTCTGGCGC AGCACCAAGG GAGTCCAACA-GCCGGC AATTAT-5'
← (Eag I) primer 8

Fig. 10

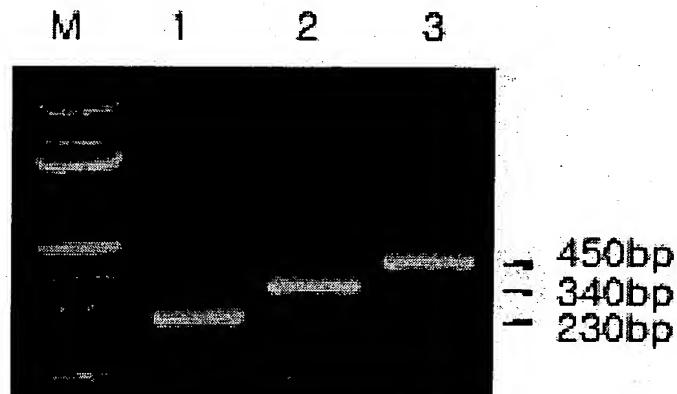


Fig. 11a

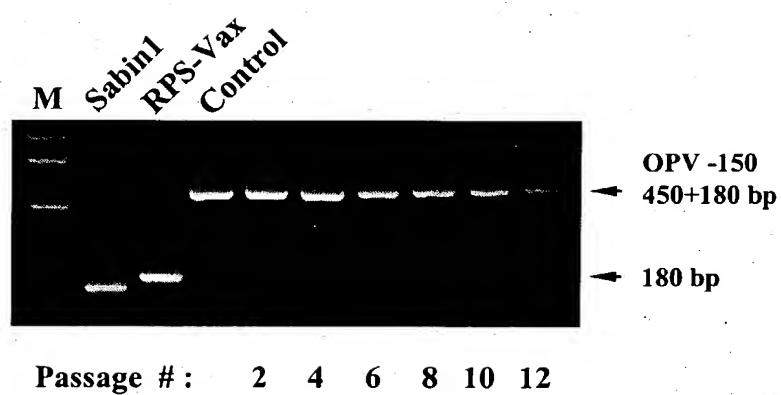


Fig. 11b

